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OIPE

## RAW SEQUENCE LISTING

DATE: 08/21/2001

PATENT APPLICATION: US/09/927,616

TIME: 12:02:14

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Output Set: N:\CRF3\08162001\I927616.raw

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3 <110> APPLICANT: Triplett, Eric W.  
 4 Herlache, Thomas C.  
 6 <120> TITLE OF INVENTION: Biological Control of Crown Gall Disease  
 8 <130> FILE REFERENCE: 960296.97273  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/927,616  
 C--> 11 <141> CURRENT FILING DATE: 2001-08-10  
 13 <150> PRIOR APPLICATION NUMBER: 60/224,929  
 14 <151> PRIOR FILING DATE: 2000-08-11  
 16 <160> NUMBER OF SEQ ID NOS: 9  
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 55 tggatcgata tacaaaagtg taatctcgcc actaacaaga gccgatccga ctccctcttac 180  
 57 tagtccggca accttagctg taagaaatat tgagtgcggg ttgtcaatcc acatcgatac 240  
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77 gcg acc ttc aag gct gct gtt ctg aag tcg aag acg aag gtc gac atc 695
78 Ala Thr Phe Lys Ala Ala Val Leu Lys Ser Lys Thr Lys Val Asp Ile
79          20          25          30
81 gga ggt agc cgt cag ggc tgc gtc gct taagtgaaca tccggcgggt 742
82 Gly Gly Ser Arg Gln Gly Cys Val Ala
83          35          40
85 gcggcaaacg taccgcgccac ttatgccctc gctttcaacg ggatgtttcg c atg gac 799
86                                     Met Asp
88 ttc gtc caa cga ttc gta atc gac cgc tct ttc cac ctc cgc tac tac 847
89 Phe Val Gln Arg Phe Val Ile Asp Arg Ser Phe His Leu Arg Tyr Tyr
90 45          50          55          60
92 agc ctc gac gcc tat cta tat cgc gca gtt gac cag gtc gcc tgg gac 895
93 Ser Leu Asp Ala Tyr Leu Tyr Arg Ala Val Asp Gln Val Ala Trp Asp
94          65          70          75
96 gca gac atc act cac aat cgc cta ttt tgg gac att tgg tca gca ttc 943
97 Ala Asp Ile Thr His Asn Arg Leu Phe Trp Asp Ile Trp Ser Ala Phe
98          80          85          90
100 atg cag ccg aga agt ctg gta gac gct gtt gag acg cta tcc gat tac 991
101 Met Gln Pro Arg Ser Leu Val Asp Ala Val Glu Thr Leu Ser Asp Tyr
102          95          100          105
104 gat ccc gac gaa gtg gcc gca gca atc gaa ggc atg tgc gag tcg ggc 1039
105 Asp Pro Asp Glu Val Ala Ala Ala Ile Glu Gly Met Cys Glu Ser Gly
106          110          115          120
108 atc atc gaa ccg gtg ggc ttg aaa gac cgc caa ttt gat cct ttg acg 1087
109 Ile Ile Glu Pro Val Gly Leu Lys Asp Arg Gln Phe Asp Pro Leu Thr
110 125          130          135          140
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113 Val Glu Leu Ser His Val Pro Gln Ala Trp Asp Tyr His Leu Val Ser
114          145          150          155
116 agt cgc atc gac tgg atc aat tat ctg gat ggg aag gac gtt aaa cgc 1183
117 Ser Arg Ile Asp Trp Ile Asn Tyr Leu Asp Gly Lys Asp Val Lys Arg
118          160          165          170
120 cag gac ctt gaa caa atg gac aag cat ttg tcg gag gag gct gtt ccg 1231
121 Gln Asp Leu Glu Gln Met Asp Lys His Leu Ser Glu Glu Ala Val Pro
122          175          180          185
124 tcg aat ttt cac aag gcc gcc aac tct cga ccg aaa tat gat ttg cca 1279
125 Ser Asn Phe His Lys Ala Ala Asn Ser Arg Pro Lys Tyr Asp Leu Pro
126          190          195          200
128 agt tta gtg ccg ctg aca gcg ttc gaa ttc aat aac tcg gcg tcc gtc 1327
129 Ser Leu Val Pro Leu Thr Ala Phe Glu Phe Asn Asn Ser Ala Ser Val
130 205          210          215          220
132 gca ttc ggt cat gag aag gca ccg ctt ccg aac gaa ctg tcg ctc gat 1375
133 Ala Phe Gly His Glu Lys Ala Pro Leu Pro Asn Glu Leu Ser Leu Asp
134          225          230          235
136 ata atc aca ttg ctc ctc aac tat gcg gcc gca aag acg gat acc gtc 1423
137 Ile Ile Thr Leu Leu Leu Asn Tyr Ala Ala Ala Lys Thr Asp Thr Val

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141 Asn Met Tyr Ala Thr Gly Glu His Leu Arg Lys Ala Val Pro Ser Gly
142          255          260          265
144 gga gcg cga cac ccc atc gaa ttc tac gtg gtt gtc ggc gat gag att 1519
145 Gly Ala Arg His Pro Ile Glu Phe Tyr Val Val Val Gly Asp Glu Ile
146          270          275          280
148 gca ggt atc gaa gct ggc gta tat cac tac aat gtt cgc cat cat cgg 1567
149 Ala Gly Ile Glu Ala Gly Val Tyr His Tyr Asn Val Arg His His Arg
150 285          290          295          300
152 ctc gat gct atc gaa ata gcg tcc acc tca ttg aaa gca ctg caa gag 1615
153 Leu Asp Ala Ile Glu Ile Ala Ser Thr Ser Leu Lys Ala Leu Gln Glu
154          305          310          315
156 gca agc tca gtg ctg ccc cga tca cgg tca aaa ccg ttc ggc ttt gct 1663
157 Ala Ser Ser Val Leu Pro Arg Ser Arg Ser Lys Pro Phe Gly Phe Ala
158          320          325          330
160 ttc att cat aca tgt cgg ttc gag cga agt atg ttt cgg tac cgc gaa 1711
161 Phe Ile His Thr Cys Arg Phe Glu Arg Ser Met Phe Arg Tyr Arg Glu
162          335          340          345
164 ccg cga agc tac cgt gtg atg cag ttt gat ctt ggg cat atc cat gcc 1759
165 Pro Arg Ser Tyr Arg Val Met Gln Phe Asp Leu Gly His Ile His Ala
166          350          355          360
168 aac gag gtt ttg gct gcc aaa atc ctc ggc ctc gat ttc agt gaa acc 1807
169 Asn Glu Val Leu Ala Ala Lys Ile Leu Gly Leu Asp Phe Ser Glu Thr
170 365          370          375          380
172 ttt tct gtg ccg gaa agc ata gtt gag agc gtc ttg acg ctc gat ccg 1855
173 Phe Ser Val Pro Glu Ser Ile Val Glu Ser Val Leu Thr Leu Asp Pro
174          385          390          395
176 ttc atc gag tcc gcg atg tca gcc ttt gtc gtc cac aga cac gag aac 1903
177 Phe Ile Glu Ser Ala Met Ser Ala Phe Val Val His Arg His Glu Asn
178          400          405          410
180 cac cat gat tgaactgcgc ccgcttctcc aactgaatct tgaagatgga 1952
181 His His Asp
182          415
184 atcccggtcc tcaaagacct cctgaccgcc gacagctttt ccttcaccga tgttgaactc 2012
186 ttgcggtaca ttccagccat tgccaagaac acccccgccc agactcggga tttggctgcc 2072
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218 ggctagagc atg agc gac gaa aac cag cat ggg ttc tat cgg act tcg ttc 3023
219      Met Ser Asp Glu Asn Gln His Gly Phe Tyr Arg Thr Ser Phe
220      420      425
222 gaa tac gca tcg atc agt tgg cgg aga atg att ccc aat gtg gct gac 3071
223 Glu Tyr Ala Ser Ile Ser Trp Arg Arg Met Ile Pro Asn Val Ala Asp
224 430      435      440      445
226 act atc gtc gtc acg ctc atc ggc gct act gca ctt cag gtg gcg tca 3119
227 Thr Ile Val Val Thr Leu Ile Gly Ala Thr Ala Leu Gln Val Ala Ser
228      450      455      460
230 aat gtt ctg atc acg ata ctg acc ctc aat atc gct ttt ctg aac ttt 3167
231 Asn Val Leu Ile Thr Ile Leu Thr Leu Asn Ile Ala Phe Leu Asn Phe
232      465      470      475
234 tgc tcg ctt atc tgc atg cac aat ctg aaa aga ggg gca aag gcc gac 3215
235 Cys Ser Leu Ile Cys Met His Asn Leu Lys Arg Gly Ala Lys Ala Asp
236      480      485      490
238 gta ttt gct gca atc gtc cgc gct gct tgc atg atg atc ggg gtc tac 3263
239 Val Phe Ala Ala Ile Val Arg Ala Ala Cys Met Met Ile Gly Val Tyr
240      495      500      505
242 ctg gcg ctt atc gcg gtc tcc gtc gcc acc ctc gaa ggt gca ccg cgt 3311
243 Leu Ala Leu Ile Ala Val Ser Val Ala Thr Leu Glu Gly Ala Pro Arg
244 510      515      520      525
246 acc caa acc att gct ttc ata gca ctg tct gcg ctc cgg ccg ttt gtg 3359
247 Thr Gln Thr Ile Ala Phe Ile Ala Leu Ser Ala Leu Arg Pro Phe Val
248      530      535      540
250 gct gga tgg aat gct tac tgt gcg gag gtt ttt ttc gcc cag gga aaa 3407
251 Ala Gly Trp Asn Ala Tyr Cys Ala Glu Val Phe Phe Ala Gln Gly Lys
252      545      550      555
254 cga caa att gtg cga agc gtc atc acg aga tcg tcg ctg atc tat gca 3455
255 Arg Gln Ile Val Arg Ser Val Ile Thr Arg Ser Ser Leu Ile Tyr Ala
256      560      565      570
258 gga gtt aat ctg ctc ttt gtc ggg ctg tcg cat ttc gct ggc act caa 3503
259 Gly Val Asn Leu Leu Phe Val Gly Leu Ser His Phe Ala Gly Thr Gln
260      575      580      585
262 aat tcg atc ata tcg ctt ctc atc ggc gta tat ctt gct ctc ttc cac 3551
263 Asn Ser Ile Ile Ser Leu Leu Ile Gly Val Tyr Leu Ala Leu Phe His
264 590      595      600      605
266 aac gcc ctg gcc tac gcc aga atc ctg ccg acc gaa tgg agg ttc agt 3599
267 Asn Ala Leu Ala Tyr Ala Arg Ile Leu Pro Thr Glu Trp Arg Phe Ser
268      610      615      620
270 cgc cag gat ttg aag gat gtc ttc tca ctt cgg aag ctt gat ctg gtc 3647
271 Arg Gln Asp Leu Lys Asp Val Phe Ser Leu Arg Lys Leu Asp Leu Val
272      625      630      635
274 gga atc ggg gca ggg ctt tct gcg tct ttt atc aac atg ctc gaa atg 3695
275 Gly Ile Gly Ala Gly Leu Ser Ala Ser Phe Ile Asn Met Leu Glu Met
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284 670      675      680      685
286 gga ctt gcg att ggg ctt gga cgc tca gtc acc gaa cgt ttg att acg 3839
287 Gly Leu Ala Ile Gly Leu Gly Arg Ser Val Thr Glu Arg Leu Ile Thr
288      690      695      700
290 ccg cgc ccg ttt ccc cgg ctg cac gtc ttg atc gcc gtt tac agc acg 3887
291 Pro Arg Pro Phe Pro Arg Leu His Val Leu Ile Ala Val Tyr Ser Thr
292      705      710      715
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295 Tyr Ser Leu Leu Cys Phe Leu Ile Tyr Val Gly Leu Ile Gly Val Ser
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307 Leu Ala Lys Ala Asp Gly Gly Lys Leu Thr His Leu Ser Ala Ile Ala
308      770      775      780
310 tac cta gcc tct gga gtg atc ctc gcg ctg gcg gcc gtc ttg ggc tcg 4127
311 Tyr Leu Ala Ser Gly Val Ile Leu Ala Leu Ala Ala Val Leu Gly Ser
312      785      790      795
314 gtt caa gcg ttg gcc atc gct ttg gtc ttg gga ccg ctg ttc ctt gca 4175
315 Val Gln Ala Leu Ala Ile Ala Leu Val Leu Gly Pro Leu Phe Leu Ala
316      800      805      810
318 atc tcc att ccc gcc gtt caa agt cga act gcc cta aat gca cta ccg 4223
319 Ile Ser Ile Pro Ala Val Gln Ser Arg Thr Ala Leu Asn Ala Leu Pro
320      815      820      825
322 aac aga taaaccgaaa gtattcgtaa ccgactccgg caggtttggt gctgactgcc 4279
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324 830
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348 attacgtgat acaggcgggt agttattc atg aga gca agc aaa aca ccg atc 4991
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**VERIFICATION SUMMARY**

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date